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## RAW SEQUENCE LISTING

DATE: 10/02/2002

PATENT APPLICATION: US/10/083,641A

TIME: 15:26:57

Input Set : A:\Seq Listing #2.txt

Output Set: N:\CRF4\10022002\J083641A.raw

3 <110> APPLICANT: HAYSTEAD, TIMOTHY A  
 5 <120> TITLE OF INVENTION: SMOOTH MUSCLE MYOSIN PHOSPHATASE ASSOCIATED KINASE  
 7 <130> FILE REFERENCE: 1579-647  
 9 <140> CURRENT APPLICATION NUMBER: 10/083,641A  
 10 <141> CURRENT FILING DATE: 2002-02-27  
 12 <150> PRIOR APPLICATION NUMBER: 60/271,436  
 13 <151> PRIOR FILING DATE: 2001-02-27  
 15 <160> NUMBER OF SEQ ID NOS: 17  
 17 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 15  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Artificial Sequence  
 24 <220> FEATURE:  
 25 <223> OTHER INFORMATION: Description of Artificial Sequence: Endogenous kinase  
 26 copurifies with SMPP-1M  
 28 <400> SEQUENCE: 1  
 29 Lys Lys Lys Arg Gln Ser Arg Arg Ser Thr Gln Gly Val Thr Leu  
 30 1 5 10 15  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 13  
 35 <212> TYPE: PRT  
 36 <213> ORGANISM: Artificial Sequence  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: Description of Artificial Sequence: human pDAPK3  
 41 <400> SEQUENCE: 2  
 42 Met Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val  
 43 1 5 10  
 46 <210> SEQ ID NO: 3  
 47 <211> LENGTH: 320  
 48 <212> TYPE: PRT  
 49 <213> ORGANISM: Artificial Sequence  
 51 <220> FEATURE:  
 52 <223> OTHER INFORMATION: Description of Artificial Sequence: ZIP Kinase  
 54 <400> SEQUENCE: 3  
 55 Met Ser Thr Phe Arg Gln Glu Asp Val Glu Asp His Tyr Glu Met Gly  
 56 1 5 10 15  
 58 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg Lys Cys Arg Gln  
 59 20 25 30  
 61 Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg  
 62 35 40 45  
 64 Leu Pro Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu  
 65 50 55 60

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67 Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His
68 65                      70                      75                      80
70 Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val
71                      85                      90                      95
73 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr
74                      100                     105                     110
76 Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu Asp Gly Val His
77                      115                     120                     125
79 Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu Lys Pro Glu Asn
80                      130                     135                     140
82 Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg Ile Lys Leu Ile
83 145                      150                      155                      160
85 Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn Glu Phe Lys Asn
86                      165                      170                      175
88 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
89                      180                      185                      190
91 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
92                      195                      200                      205
94 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu Thr Lys Gln Glu
95                      210                      215                      220
97 Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe Asp Glu Glu Tyr
98 225                      230                      235                      240
100 Phe Ser Ser Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu
101                      245                      250                      255
103 Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln Ser Leu Glu His
104                      260                      265                      270
106 Ser Trp Ile Lys Val Arg Arg Arg Glu Asp Gly Ala Arg Lys Pro Glu
107                      275                      280                      285
109 Arg Arg Arg Leu Arg Ala Ala Arg Leu Arg Glu Tyr Ser Leu Lys Ser
110                      290                      295                      300
112 His Ser Ser Met Pro Arg Asn Thr Ser Tyr Ala Ser Phe Glu Arg Phe
113 305                      310                      315                      320

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119 &lt;210&gt; SEQ ID NO: 4

120 &lt;211&gt; LENGTH: 13

121 &lt;212&gt; TYPE: PRT

122 &lt;213&gt; ORGANISM: Artificial Sequence

124 &lt;220&gt; FEATURE:

125 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: rat DAP-like kinase

127 &lt;220&gt; FEATURE:

128 &lt;221&gt; NAME/KEY: Unsure

129 &lt;222&gt; LOCATION: (6), (9)

130 &lt;223&gt; OTHER INFORMATION: Xaa can be any amino acid

132 &lt;400&gt; SEQUENCE: 4

W--&gt; 133 Met Leu Leu Asp Lys Xaa Ile Phe Xaa Arg Pro Ile Gln

134 1 5 10

137 &lt;210&gt; SEQ ID NO: 5

138 &lt;211&gt; LENGTH: 13

139 &lt;212&gt; TYPE: PRT

140 &lt;213&gt; ORGANISM: Artificial Sequence

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```

142 <220> FEATURE:
143 <223> OTHER INFORMATION: Description of Artificial Sequence: D-glycerate
dehydrogenase
145 <220> FEATURE:
146 <221> NAME/KEY: Unsure
147 <222> LOCATION: (8), (10), (11) and (13)
148 <223> OTHER INFORMATION: Xaa can be any amino acid
150 <400> SEQUENCE: 5
W--> 151 Met Thr Ile Ala Gln Asn Leu Xaa Tyr Xaa Xaa Ile Xaa
152      1              5              10
155 <210> SEQ ID NO: 6
156 <211> LENGTH: 1093
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: Putative nucleotide
162      sequence of smooth muscle MYPT-Kinase
164 <220> FEATURE:
165 <221> NAME/KEY: Unsure
166 <222> LOCATION: (2), (7), (37), (39), (1056), (1081) and (1092)
167 <223> OTHER INFORMATION: N can be A, C, G or T
169 <400> SEQUENCE: 6
W--> 170 gntatgnata tcggtttaat cggccggagc tcgcccncng ggcagctgga ctccctctca 60
171 gacctccttc tttctcgccc tcagcacggg attaacctca cttgactgtt cttgggtccc 120
172 cgggtgccggg ccagcgtcct ctccctcaag gcaatcccca agtgtctgtc atgaggctct 180
173 ttgggcagtt ctgttggtgt gggaaacctg ggaacagatg cacagaggct ggggtacaga 240
174 gtectgcctt cctctgggtc tgcagcgctt agctgttcct tccccacag cggccagttc 300
175 gccatcgtgc gcaagtgccg gcagaaggcg accggcatgg agtacgcggc caagttcata 360
176 aagaagcggc gcctgccgtc cagccggcgc ggtgtgagcc gtgaggagat cgagcgcgag 420
177 gtgagcatcc tgcgcgagat ccgccacccc aacatcatca cgctgcacga tgtgttcgag 480
178 aacaagacag atgtggtgct gatcttgag ctggtgtccg gcggcgaaact tttcgacttt 540
179 ctggctgaga aggatcactg acagaggatg aggccacgca gttcctcaag cagatcctgg 600
180 acggtgtcca ctacctgcac tccaagcgca tcgcgcactt tgacctgaag ccggagaaca 660
181 tcatgttgct ggacaagcat gcagccagcc cacgcattaa gctcatcgac tttggcatcg 720
182 cgcacaggat cgaggccggg agcgagttca agaacatctt tggcacgcca gaggctcgcg 780
183 gtgaggggca ggtgtgggca ccaccgata gggtagattt tgcacggcct tggcctgacc 840
184 tgcctcaaca atcctgtctt ccacagcccc tgagattgta aactatgaac cacttggtct 900
185 ggaagctgat atgtggagca tcggcgatc cactacatc ctgtgagtg ctgagatggg 960
186 caggggcctc agactgtacc tgctagaggc ccagggatca gggtggcac ctctgcaaac 1020
W--> 187 tgcaaact ggggctgaga gatgtccctg ggaacnctgg atatgcctgg gccccaccaa 1080
W--> 188 ngtaggacca tnc                                     1093
191 <210> SEQ ID NO: 7
192 <211> LENGTH: 34
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino acid
sequence of rat
198      aorta smooth muscle MYPT-kinase
200 <220> FEATURE:
201 <221> NAME/KEY: Unsure

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202 <222> LOCATION: (1), (3) and (13)

203 <223> OTHER INFORMATION: Xaa can be any amino acid

205 <400> SEQUENCE: 7

W--> 206 Xaa Met Xaa Ile Gly Leu Ile Gly Arg Ser Ser Pro Xaa Gly Gln Leu  
207 1 5 10 15  
209 Asp Ser Leu Ser Asp Leu Leu Leu Ser Arg Pro Gln His Gly Ile Asn  
210 20 25 30  
212 Leu Thr

216 <210> SEQ ID NO: 8

217 <211> LENGTH: 22

218 <212> TYPE: PRT

219 <213> ORGANISM: Artificial Sequence

221 <220> FEATURE:

222 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino acid  
sequence of rat

223 aorta smooth muscle MYPT-kinase

225 <400> SEQUENCE: 8

226 Leu Phe Leu Gly Pro Arg Cys Arg Ala Ser Val Leu Ser Leu Lys Ala  
227 1 5 10 15  
229 Ile Pro Lys Cys Leu Ser  
230 20

233 <210> SEQ ID NO: 9

234 <211> LENGTH: 125

235 <212> TYPE: PRT

236 <213> ORGANISM: Artificial Sequence

238 <220> FEATURE:

239 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino acid  
sequence of rat

240 aorta smooth muscle MYPT-kinase

242 <400> SEQUENCE: 9

243 Gly Ser Leu Gly Ser Ser Val Val Val Gly Asn Leu Gly Thr Asp Ala  
244 1 5 10 15  
246 Gln Arg Leu Gly Tyr Arg Val Leu Pro Ser Ser Gly Ser Ala Ala Leu  
247 20 25 30  
249 Ser Cys Ser Phe Pro His Ser Gly Phe Ala Ile Val Arg Lys Cys Lys  
250 35 40 45  
252 Gly Thr Gly Met Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg Leu  
253 50 55 60  
255 Pro Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu Val  
256 65 70 75 80  
258 Ser Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His Asp  
259 85 90 95  
261 Val Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val Ser  
262 100 105 110  
264 Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Asp His  
265 115 120 125

268 <210> SEQ ID NO: 10

269 <211> LENGTH: 28

270 <212> TYPE: PRT

271 <213> ORGANISM: Artificial Sequence

273 <220> FEATURE:

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Input Set : A:\Seq Listing #2.txt

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274 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
275     acid sequence of rat aorta smooth muscle
276     MYPT-kinase
278 <400> SEQUENCE: 10
279 Gln Arg Met Arg Pro Arg Ser Ser Ser Arg Ser Trp Thr Val Ser
280  1           5           10           15
282 Thr Thr Cys Thr Pro Ser Ala Ser Arg Thr Leu Thr
283     20           25
286 <210> SEQ ID NO: 11
287 <211> LENGTH: 55
288 <212> TYPE: PRT
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
293     acid sequence of rat aorta smooth muscle
294     MYPT-kinase
296 <400> SEQUENCE: 11
297 Ser Arg Arg Thr Ser Cys Cys Trp Thr Ser Met Gln Pro Ala His Ala
298  1           5           10           15
300 Leu Ser Ser Ser Thr Leu Ala Ser Arg Thr Gly Ser Arg Pro Val Ala
301     20           25           30
303 Ser Ser Arg Thr Ser Leu Ala Arg Gln Ser Ser Ser Val Arg Gly Arg
304     35           40           45
306 Cys Gly His His Pro Ile Gly
307     50           55
310 <210> SEQ ID NO: 12
311 <211> LENGTH: 18
312 <212> TYPE: PRT
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
317     acid sequence of rat aorta smooth muscle
318     MYPT-kinase
320 <400> SEQUENCE: 12
321 Ile Leu His Gly Leu Thr Cys Leu Asn Asn Pro Val Phe His
322  1           5           10           15
324 Ser Pro
328 <210> SEQ ID NO: 13
329 <211> LENGTH: 4
330 <212> TYPE: PRT
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
335     acid sequence of rat aorta smooth muscle
336     MYPT-kinase
338 <400> SEQUENCE: 13
339 Asp Cys Lys Leu
340  1
343 <210> SEQ ID NO: 14

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/083,641A

DATE: 10/02/2002  
TIME: 15:26:58

Input Set : A:\Seq Listing #2.txt  
Output Set: N:\CRF4\10022002\J083641A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 6,9  
Seq#:5; Xaa Pos. 8,10,11,13  
Seq#:6; N Pos. 2,7,37,39,1056,1081,1092  
Seq#:7; Xaa Pos. 1,3,13  
Seq#:17; Xaa Pos. 15,18